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GenCore version 5.1.4 p5_4578 Copyright (c) 1993 - 2003 Compugen_Ltd.
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OM protein - protein search, using sw model

April 1, 2003, 08:45:46; Search time 47 Seconds (without alignments) 918.391 Million cell updates/sec Run on:

Title: Perfect score:

US-09-768-781-3 2316 1 MDRVYEIPEEPNVDPVSSLE......RTRVENSEPPFETEARQSVV 449 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	McLeod syndrome-as	hypothetical prote			hypothetical prote			- ⊢	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	NADH2 dehydrogenas	ferric anquibactin	NADH2 dehydrogenas	brain-specific ang	probable membrane	probable transport			transmembrane tran	hypothetical prote		hypothetical prote	probable membrane	hypothetical prote	related to SREBP c	NADH2 dehydrogenas	hypothetical prote	NADH2 dehydrogenas
SUMMARIES		139294	T32470	E75203	T02024	A96825	D90567	A86299	B97305	T11039	T17163	T17166	T17172	G82880	T17169	T00026	AH0600	F90739	H85589	H64817	D75104	G96595	T21603	T25628	S53040	T15322	T48829	863658	\sim	T17181
	DB	7	~	~	~	7	7	~	~	~	~	7	ď	~	~	~	~	N	~	~	~	N	~	~	~	~	N	~	~	7
	Length	444	439	382	745	783	508	785	461	498	459	459	459	341	459	1584	740	741	741	786	503	2143	313	378	405	521	1154	474	438	459
æ	Query Match	39.6	5.6	5.5	5.2	5.1	4 .	4.9	4.7	4.7	4.7	4.6	4.6	4.6	4.6	4.6	4.5	4.5	4.5	4.5	4.5	4.5	4.	4.4	4.4	4.4	4.4	4.4	4.4	4.4
	Score	918	129	120.5	119.5	•		112.5	109.5	109.5	108	101	107	106.5	105.5	105.5	0	104.5	104.5	104.5	103.5	103.5	102.5	102.5	102.5	102.5	102.5	0	101.5	101
	Result No.	٦	7	m	4	'n	9	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	53

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NADH2 dehydrogenas	hypothetical prote	H+-transporting tw	oligopeptide perme	peptide ABC transp	hypothetical prote	probable Na+/H+ an	hypothetical prote	conserved hypothet	probable K+ transp	nicotinic acetylch	K+ transport prote	TCM10 protein - ye	probable calcium-t	hypothetical prote	hynotherical profe
7144	4113	02157	C86565	D72059	D86304	G90476	T19008	C69309	F71360	138056	C70190	S61147	T39030	T26917	G83707
E	8	O)													
2 T1.	2 3	7	0	7	~	7	7	~	~	7	7	~	N	~	S
~	~	ч	493 2	493 2	570 2	599 2	346 2	370 2	575 2	423 2	443 2	611 2	1033 2	345 2	372 2
459 2	483 2	264 1								4.3 423 2			-		
4.4 459 2	4.4 483 2	4.3 264 1	4.3	4.3	4.3	4.3	4.3	4.3	4.3		4.3	4.3	4.3	4.2	6.4

ALIGNMENTS

	RESULT 1
	100000
	132294
	McLeod syndrome-associated protein XK - human
_	N;Alternate names: probable membrane transport protein
	C;Species: Homo sapiens (man)
	C;Date: 16-Feb-1996 #sequence revision 16-Feb-1996 #text change 01-Dec-2000
	C; Accession: 139294; S69126
	R;Ho, M.; Chelly, J.; Carter, N.; Danek, A.; Crocker, P.; Monaco, A.P.
	Cell 77, 869-880, 1994
_	A; Title: Isolation of the gene for McLeod syndrome that encodes a novel membrane transpor
	A; Reference number: A54300; MUID: 94273191; PMID: 8004674
	A; Accession: I39294
	A;Status: preliminary
	A; Molecule type: mRNA
	A;Residues: 1-444 <res></res>
	A;Cross-references: EMBL:Z32684: NID:G515872: PID:G515873
	R:Khamlichi, S.: Bailly, P.: Blanchard, D.: Gooseens, D.: Cartron, J.P.: Bertrand, O.
	Bur. J. Biochem. 228. 931-934 1995
	A: Title: Purification and partial characterization of the ervthrocyte Kx protein deficier
	A:Reference number: 869126; MuID:95255304; PMID:7737196
	A:Accession: S69126
	A; Status: preliminary
_	A:Molecule type: protein
	A:Residnes: 7-23 ckHA>
_	Ciganatics
	D.Comp. CDB.YK
	A:Cross references GDR-120499 OMTM-214850
	1. Man medition: Yn21 2 - Yn21 1
	Child Postitudis April - April -
	Cineywords: prosproprocein; transmembrane procein
	Query Match 39.6%; Score 918; DB 2; Length 444;
	Matches 178; Conservative 80; Mismatches 134; Indels 10; Gaps 4;
	ON 33 PDESTIFETELYCGEAAGALVMUDTVPRIGEFFWPMTVFFGFFFFFGTMIOLFFLFFUHDIL 92
	Db 3 PPASVIASVELEVAETTAALSLSSTYRSGGRRMMOALTLIFSLLPCALVOLTLIFVHEDL 62
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5.2%; Score 120.5; DB 2;
22.7%; Pred. No. 0.018;
tive 56; Mismatches 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Gene: rbohA
C,Keywords: calcium binding; membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     240 VLCITIWRTLEITSRLLILVLFSA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-745 <KEL>
                                                                                                                                                                                                                               Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: Z14499
                                                                                                                                                                                                          Best Local Similarity
  A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEMLL 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: T02024
                                                                                                                                       A;Gene: PAB2250
                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396
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C;Species: Pyrococcus abyssi
C;Jote: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C;Accession: E75203
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: EMBL:AF026213; PIDN:AAB71305.1; GSPDB:GN00028; CESP:F08F1.5
Experimental source: strain Bristol N2; clone F08F1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                            hypothetical protein FO8F1.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: Ti2470
R;Pulton, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 ------RKCFSKMVEAERDATLLRFFEAFLESAPOLIIQGSIAASYFONYYQTGTY 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 IWRTLEITSRLLILVLFSATLKLKAVPFLVLNFLILFEPWIKFWRSGAQMPNNIEKNFS 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              305 RVGTLVVLISVTILYAGINFSCWSALQLRLADRDLVDKGQNWGHMGLHYSVRLVENVIMV 364
240 IILINFFSFFLYPWILFWCSGSPFPENIEKALSRVGTTIVLCFLTLLYTGINMFCWSAVO 299
                                                332 LRLADRDLVDKGONWGHMGLHYSVRLVENVIMVLVFKFFGVKVLLNYCHSLIALQLIIAY 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               185 TYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYKIRLGPLEVLCIT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 PLSLFMHLIL--LGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKMLIDGEEVLIEWEV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 PYWLYFQAAS-----LLLSIISISWSVVVQNRSLRMIR--DDKVNIWFHEAVLQF
                                                                        155 GHSIRTLAMHRNAYKRMSQ-----IQAPLGSVPQL-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98; Indels 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: X
A;Introns: 20/1; 72/3; 137/3; 184/2; 263/3; 289/3; 339/3; 369/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F08F1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 439;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    365 LVFKFFGVKVLLNYCHSLIALQLIIAYLISIDFMLLFFQYLHPLR 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVCWLLPLSLNTFPYIEKVQVGVPISFIAGIAIMMYYQFFHPNR 384
                                                                                                                                         392 LISIDFMLLFFQYLHPLRSLFTHNVVD----YLHCVC--CHQ 427
                                                                                                                                                                360 CTAILFMLVFYQFFHPCKKLFSSSVSEGFQRWLRCFCWACRQ 401
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: The sequence of C. elegans cosmid FO8F1. A; Reference number: 221174
A; Accession: T32470
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 129; DB 2; ; Pred. No. 0.004; 62; Mismatches 5
                                                                                                                                                                                                                                                                                                                                                                                                              September 1997
                                                                                                                                                                                                                                                                                                                                                                                         R, Pulton, B. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 5.6%;
Local Similarity 19.4%;
les 67; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-439 <FUL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: CESP: F08F1.5
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Cytochrome b245 beta chain homolog rbohA - rice (fragment)
N;Alternate names: intrinsic plasma membrane protein RbohAOsp
C;Species: Oryza sativa (rice)
C;Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 23-Jul-1999
C;Accession: T02024
R;Keller, T; Damude, H.G; Werner, D; Doerner, P; Dixon, R.A; Lamb, C.
submitted to the EMBL Data Library, July 1997
A;Description: A plant homolog of the neutrophil NADPH oxidase gp91phox subunit gene enc
A;Molecule type: DNA
A;Residues: 1-382 «KAW»
A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49076.1; PID:e15149'
A;Experimental source: strain Orsay
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 : || :: :| : :| : || || || || || || 313 RKVLVAYRRSSLAIG---GLNAVQNVSTFLGGLFFGLAYSLGELHSIITVNLGLASFLPF 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72 SFFM----FSSIMVQLTLIFVHRDLAKDKPLSLFWHLILLGPVIRCLEAMIKYLTLWKKEE 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 QEEPYVSLTRKKMLIDGEEVL----IEWEVGHSIRTLAMHRNAYKRMSQIQAFLGSVP 182
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                                                                        STFLYC-GEAASALYMVRIYRKNSETYRMTY-TFSFFWFSSIMVQLTLIFVHRDLAKDKP 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49 SFILARAFSSLFSGLL-----LEKDK------RLIYLGSVTMAGNALIVHL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 QLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLA---IQIKYDDYKIRLGPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 382;
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C;Genetics:
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us-09-768-781-3.rpr

6 :	IEWEVGHSIRTLAWHRNAYKRMSQIQAFLGSVPQLTYQLYVSLISAEVPLGRVVL	234 PKRNPKEKYLSKAETLVFFIFLLIIGITIESYDVNSSVSVFAIGIMFPRQGKT
8 8	125 ELWQLETLLLDQKDITMNYSQALSQYLSQALSQNLAGERKKKSSIRKIS 170 205 MVFSLVSVTYGATLCNMLAIOIKYDDYKTRIGPLEVICTTIWRTHEITSRIJII. 258	OY 336 DRDLVDKGONWGHMGLHYSVRLVENVIMVLVFKFFGV 372 Dh 287 HFMLIOPLSVPTHFFVLPVFGYTGFFFSTTALTKRFYLGTVIIVLVTTAGFFGYJSAC 346
, 임		373CHSLIALQLIST VERY LOTTER LATER L
ò	259 VL-PSATLKLKAVPPLVLNPLIILPEPWIKFWRSGAQMPNNIEKNFSRVGTLVV 311	Db 347 MYLKIPKKYWLFLPTILSVKGHVGLLLDSNYSEKKWWTTTIHDMMVAALVITTLVSGVL 406
qq	213 VMGYCVTTAKGAAETLKLNMAIILLPVCRNTITWLRSTRAARALPFDDNINFHKTIAAAI 272	Qy 395 IDFWLLFFQYLHPLRSLFTHNVVDYLHCVCC 425
중 음 중	312 LISVTILYAGINFSCWSALQLRLADRDLVDKGQNWGHMYSVRLVENVIMVLV 366 ::: : : : ::: 273 VVGI-ILHAGNHLVCDFPRLIKSSDEKYAPLGQYFGEIKPTYFTLVKGVEGITGVIMVVC 331	Db 407 ASFLLKTREKDFAYEKTSLESHNTNEELRILSC 439
<u>ځ</u> ۾	367 FAYLISID 396 : : 3 332 MIJAFTLATRWFRRSLVKLPRPFDKLTGFWAFW-YSHHLFIJVYTALIVHGECLYLJHVW 390	RESULT 6 D90567 hypothetical protein MYPU_4440 [imported] - Mycoplasma pulmonis (strain UAB CTIP) C:Species: Mycoplasma pulmonis
5 5	397 EMLLFROYL 405	C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001 C;Accession: D90567 R;Chanbaud, I.; Hellig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I
3		Nuclet, Actual res. 27, 419-413-7, 2001 A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulr A;Reference number: A99512; MUID:21267165; PMID:11353084
A968	LT 5 255 255	A;Accession: D90567 A;Scatus: pyeliminary A;Actus: pinary
C; Sp	Lifelical process, 1874-19 (imported) - Arabidopsis Charlana edies: Arabidopsis thallana (mouse-ear cres) te: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001	A; MULGCULE LYPE: DNA A; Readdudes: 1-508 «KUR» A; Cross-references: GB:AL445566; PID:g14089858; PIDN:CAC13617.1; GSPDB:GN00153
C, Ac R, Th Chi	cession: A96825 eologia, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, n. C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; n, N.F.; Hughes, B.; Huizar, L.	A,Experimental source: strain UAB CTIP C,Genetics: MYPU 4440 A,Genetic code: SGC3
Natu A;Au C.A.	re 408, B16-820, 2000 thors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. ; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, o. M.; Roonev, T.; Rowlev, D.; Sakano, H.	Query Match 4.9%; Score 113.5; DB 2; Length 508; Best Local Similarity 18.3%; Pred. No. 0.096; Matches 81; Conservative 90; Mismatches 159; Indels 113; Gaps 20;
A; Au ker, A; Ti	thors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. Lels: Sequence and analysis of chromosome l of the plant Arabidopsis. Ference number: A86141: MUID:21016719: PMD:11130712	PFSILESTFLYCGEAASALYMVRIYRKNSETYRMTYTFSF
A; St. A; Mo	cession: A96825 Blus: preliminary lecule type: DNA	78 SIMVQLTLIFVHRDLAKDKP : : : : 148 EILYSVYMLYNRRVERDHL
A Ge A	A;Cross-references: GB:AE005173; NID:g4835769; PIDN:AAD30236.1; GSPDB:GN00141 C;Genetics: A;Gene: T8K14.18 A;Map position: 1	138 RKKMLIDGEEVLIEWEVGHSIRTLAMHRNAYKRMSOIQAFL
888	Query Match S.1%; Score 118.5; DB 2; Length 783; Best Local Similarity 19.6%; Pred. No. 0.06; Matches 89; Conservative 69; Mismatches 166; Indels 129; Gaps 19;	Qy 179 GSVPQLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYD 229 :
දු ද	73 FFMFSSIMVOLTLIFVHRDLAKDKPLSLFMHLILLGPVIRCLEAMIKYLTLW 124	Oy 230 DYKIRLGPLEVICITIMRTLEITSRLLILULFSATLKLKAVPFLVINFL-IILFEPW 285 1
දි දි	125 KKBEQEEPYVSLTRKKMLIDGEEVLIEWEVGHSIRTLAMHRNAYKRMSQIQAFL 178 	Qy 286 IKFWRSGAQMPNNIEKUFSRVGTLVVLISVTILYAGINFSCWSALQLRLADRDLVDKGQN 345
ර සි	179 GSVPQLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKXDDYKIRL 235 125 GLLSFASLMLFIPLFGIKEDYFTFFLVLLVTLSNTASPVVVRSIADWKLNTCEI 178	Qy 346 WGHMGLHYSVRLVENVIMVLVFKFFGVKVLLNYCHSLIALQLIIAYLISIDFMLLFFGYL 405
දි දි	236 GPLEVLCITIWRTLEITSRLLILVLFSATLKLKAVPFLVLNFLIILFEPWIKFWRS 291	Qy 406 HPLRSLFTHNVVDX 419 bb 453 KSLSTLKTEKKPWTFNKKNIFDX 475
ò	292 GAQMPNNIEKNFSRVGTLVVLISVTILYAGINFSCWSALQLRLA 335	RESULT 7

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eugametos mitochoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - Chlamydomonas eugametos C;Species: mitochondrian Chlamydomonas eugametos C;Species: mitochondrian Chlamydomonas eugametos C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 03-Jun-2002 C;Accession: T11039
R;Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.
R;Denovan-Wright, E.M.; Nedelcu, A.M.; Lee, R.W.
A;Title: Complete sequence of the mitochondrial DNA of Chlamydomonas eugametos. A;Reference number: Z17244; MUID:98145434; PMID:9484440
                                                                                                 PID:g15026374; GSPDB:GN00168
ATCC824
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;Cross-references: EMBL:AF008237; NID:g2865253; PID:g2865257; PIDN:AAC39340.1
                                                                                                                                                                                                                                                                                                                                                                                                                                       ----QLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQI 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KY----DDYKIRLGPLEVLCITIWRT-LEITSRLLILVLFS------ATLKLKA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               270 V----PFLVLNFLIILFEPWIKFWRSGAOMPNNIEKNFSRVGTLVVLISVTILYAGINFS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77 -SSIMVQLTLIFVHRDLAKDK--PLSL-FMHLILLGPVIRÇLEAMIKYLTLWKKEEQEEP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      328 VIIISAFVWVGF-IIWAQPLIGFFLKDAQLVSKTVSAFRIVISMLPLLG--IYYVAIYYY 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 TYQLYVSLISAEVPLGRVVLMVFSLVSVTYGA-----TLCNMLAIQIKYDDYKIRL- 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YVSLTRKKMLIDGE-----EVLIEWEV------GHSIRTLAMHRNAYKRMSQIQAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CWSALQLRLADRDLVDKGQNWGHMGLHYSVRLVENVIM-----VLVFKFFGVK-VLLNYC
                                                                                                                                                                                                                                                               Length 461;
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
                                                                                                                                                                                                                                                        4.7%; Score 109.5; DB 2;
20.5%; Pred. No. 0.19;
tive 79; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89;
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                              A,Molecule type: DNA
A,Residues: 1-461 <KUR>
A,Cross-references: GB:AE001437; PIDN:AAK81229.1;
A,Experimental source: Clostridium acetobutylicum
C,Genelics:
A;Gene: CAC3295
                                                                                                                                                                                                                                                                                                                                                                                               33 FPF-SILFSTFLYCGEAASALYMVRIY-RKNSETYR---
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4.7%; Score 109.5; D
Best Local Similarity 22.1%; Pred. No. 0.2;
Matches 64; Conservative 46; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----PLTDIIVILTSVYFIRRAFK 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      380 HSLIALQLIIAYLISIDFMLLFFQ
                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 20.5%;
Matches 91; Conservative
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A;Status: preliminary
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                       hypothetical protein F309.18 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: A86299
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.H.; C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.;
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; K.M.; Sun, H.; Tallon, A;Title: Sequence and analysis of chromosome lof the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: A8629
A;Accession: A8620
A;Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: B97305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable cation efflux pump (multidrug resistance protein) [imported] - Clostridium acet C; Species: Clostridium acetobutylicum (c; Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #sequence_revision 14-Sep-2001 #secuence_revision 14-Sep-2001 #secuence_revision 14-Sep-2001 #secuence_revision 14-Sep-2001 #secuence, G; Cmelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, Daly, M.J.; Bennett, G.N.; Koonin, B.V.; Smith, D.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:AE005172; NID:g4966359; PIDN:AAD34690.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           193 ---PIYTIVLSFISGTMTADIFIXSFATGVIILTNRFLASWLPKRNPKEKYLSKAETLAF 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----GHIGL---VLLDSN----LMYKKWPTPVV----HDMFVAALVIMTLLSGVIT 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 TLIF-VHRDLAKDKPLSLFWHLILLGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKML 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 AFVFLIGLEIDLD-----PMKRNLKNSIVITLGSLVISGIIWL-----PFLWFLIRFWO 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDGE--------EVLIEWEVGHS-IRTLAMHRNAYKRMSQIQAFLGS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240 -VLCITIWRTLB---ITSRLLILV---LFSATLK-----LKAVPFLVLNFLIILFEFWIK 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              250 IILILIIALTIESSNLNSTLFVFIIGLMFPREGKTYRTLIORLSYPIHEFVLPVYFGYIG 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30 LVFSQFFYLFLKPCGQAGPVAQILAGIVLSLLTIIRKVHEFFLQKDSASYYFFSFLLRT 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 ILFSTFLY-----CGEAAS-----ALYMVRIYRKNSETYRMTYTFSFFMFSSIMVQL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 VPQLTYQLYVSLISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYKIRLGPLE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 4.9%; Score 112.5; DB 2; Best Local Similarity 19.7%; Pred. No. 0.19; Matches 89; Conservative 84; Mismatches 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA A; Residues: 1-785 <STO> A; Cross-reference: C; Generic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Map position: 1
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Clacesion: T1166
R;Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.O.; Hu, H.G.; X.
Int. J. Primatol. 18, 305-320, 1997
A;Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences A;Reference number: 218709
A;Recession: T1716
A;Recession: T1716
A;Recession: T1716
A;Recence complex: DNA
A;Residues: 1-459 <WANY
A;Residues: 1-459 <WANY
Cross-references: EMBL:U92957; NID:g2290441; PID:g2290444; PIDN:AAD08826.1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Reywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / Match 4.6%; Score 107; DB 2; Length 459; Local Similarity 19.2%; Pred. No. 0.3; nes 80; Conservative 71; Mismatches 143; Indels 122;
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R; Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xi Tint. J. Primatol. 18, 305-320, 1997
A; Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences. A; Reference number: Z18709
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A; Residues: 1-459 <WAN>
A; Cross-references: EMBL:U92956; NID:g2290437; PID:g2290440; PIDN:AAD08823.1
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti
C;Species: mitochondrion Pygathrix bieti
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002
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                                                                                                     91 LLTSALPPICIMVMRTFKGYITFLLLEIVIYGALNVLDLLGFYLLFEASLILFFLL--- 147
                                                                                                                                                                                                                                                         YG----ATLCNMLAIQIKYDDYKIRLGPLEVLCITIWRTLEITSRLLILVLFSATLKLKA 269
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                                                                                                                                                                                                                                                                                                                                                                                                         -----TTTW--
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4.7%; Score 108; DB 2; Length 459;
Best Local Similarity 19.2%; Pred. No. 0.25;
Matches 80; Conservative 71; Mismatches 143; Indels 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             239 PEAHVAAPTAGSVLLAGVILKIGGIGFIRFMIPILPSFTASIFPLVCCMC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ALQLITAYLISIDFMLLFFQYLHPLRSLFTHNVVDYLHCVC 424
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-----SFTGAIVLMIAHGLTSSMLFCLANS 332

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Nubriz dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti mil C,Species: mitochondrion Pygathrix bieti C,Species: mitochondrion Pygathrix bieti C,Species: 19-May-2000 #text_change 03-Jun-2002 B,May-2000 #text_change 03-Jun-2002 B,May-2000 #text_change 03-Jun-2002 B,Mang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.O.; Hu, H.G.; X. Int. J. Primatol. 18, 305-320, 1997 A,Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences A,Reference number: 218709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-459 <WAN>
A;Cross-references: EMBL:U92959; NID:G2290449; PID:G2290452; PIDN:AAD08832.1
A;Cross-references: EMBL:U92959; NID:G129049; Did:G10450452; PIDN:AAD08832.1
C;Superfamily: NADH debyddrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 FSILFSTFLYCGEAASALYMVRIYRKNSETYRMTYTFSFFMFSSIMVQLTLIFVHRDLAK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.6%; Score 107; DB 2; Length 459;
19.2%; Pred. No. 0.3;
tive 71; Mismatches 143; Indels 1
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Best Local Similarity 19.2'
Matches 80; Conservative
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RESULT 11 T17166 TADRI2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti mit C;Species: mitochondrion Pygathrix bieti

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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 [similarity] - Pygathrix bieti
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;Molecule type: DNA
;Residues: 1-341 <GLA>
;Cross-references: GB.AE002150; GB.AF222894; NID:g6899515; PIDN:AAF30929.1; GSPDB:GN001
;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                               291 VSHMALVIMASLIQTPW------SPICAIVIMIAHGLISSMLFCLANS 332
                                                                                                                                                                                                                                                323 NPSCWSALQLRLADRDLVDK------GQNWGHMGLHYSVRLV-ENVIMVLVFKFFGV 372
                                                                                                                                                                                                                                                                                  391
DKPLSLPMHLILLGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKMLIDGEEVLIEWEV 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 GVIVNFLSVALGASİAKNLPKLANAYVS----RYTYGSIEPQQESFFIALVLIIIGL-LI 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              --DLAKDKPLSLFMH----LILLGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKMLID 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEEV-LIEWEVGHSI-RTLAMHRNAYKRMSQIQAFLGSVPQLTYQLYVSLISAEVPLGRV 202
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 VLPNFKKIQIVSSNQDLANQLGINVKLTSGLL----LVAICLMVGASYSLNGNLIFIGLM 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SATLKLKAVPFLVLNFLILLFEPWIKFWRSGAQMPNNIEKNFS----RVGTLVVLISVTI 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---GSVISNNRFKSAAISSGCCGSLIYMLSFLL 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 ILFSTFL--YCGEAASALYMVRIYRKN--SETYRMTYTFSFFMFSSIMVQLTLIFVHR-- 90
                                                                                                                                                  241 YGMMRLTSILNPLTEYMAY------PFLMLSLWGMIMTSSTCLROTDLKSLIAYSS
                                                                                                                                                                                    270 VPFLVLNFLIILFE-PWIKFWRSGAQMPNNIEKNFSRVGTLVVLI-----SVTILYAGI
                                                                                                                                                                                                                                                                            333 NYERTHS-RIMLLSRGLQTLLPLMAFWWFAANLINLALPPTINLIGELLVMMTSFSWSHV
                                                        155 GHSIRTLAMHRNAYKRMSQIQAFLGSVPQLTYQLYVSLISAEVPL-GRVVLMVFSLVSVT
                                                                                                                      YG----ATLCNMLAIQIKYDDYKIRLGPLEVLCITIWRTLEITSRLLILVLFSATLKLKA
                                                                                                                                                                                                                                                                                                            373 KVLLNYCHSLIALQLIIAYLISIDFMLLFFQ-----YLHPLRSLFT-HNVVDYLH 421
                                                                                                                                                                                                                                                                                                                                  ::| | | :: | | | :: | | 392 TIMLT-----GLNMLITALYSL-YMLVTTQRGTLTSHIINMKPSFTRENMLMFMH 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4.6%; Score 106.5; DB 2; Length 341; 22.3%; Pred. No. 0.24; ive 52; Mismatches 116; Indels 79;
                              ---PLLTĽTAQKL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   306 FIKILNFDSQWLNLAIPL 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            318 LYAGINF-SCWSALQLRL 334
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Query Match
Best Local Similarity 22.3%
Matches 71; Conservative
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A, Genetic code: SGC3
                           174 ---LNI---
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Nylternate names: BAII protein
NyAlternate names: BAII protein
NyAlternate names: BAII protein
Cipacies: Homo sapiens (man)
Cipacies: Toolog
Rinateuchi, T.; Urano, T.; Kimura, Y.; Kiyono, K.; Tatsumi, K.; Yoshic
Bibmitted to the EMBL Data Library, June 1997
A;Reference number: Z14064
A;Accession: T00026
A;Accession: T00026
A;Accession: T00026
A;Accession: L1584 AIIS
A;Accession: L1584 AIIS
A;Accession: Competition (man)
A;Experimental source: EMBL:AB005297; NID:d1175078; PID:d1024528
C; Species: mitochondrion Pygathrix bieti
C; Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 03-Jun-2002
C; Joacesion: T17169
R; Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; X. Int. J. Primatol. 18, 305-320, 1997
A; Title: A phylogeny of Chinese leaf monkeys using mitochondrial ND3-ND4 gene sequences A; Reference number: Z18709
A; Accession: T17169
A; Statues: preliminary
A; Molecule type: DNA
A; Residues: 1-459 < WAN>
                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:U92958; NID:g2290445; PID:g2290448; PIDN:AAD08829.1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155 GHSIRTLAMHRNAYKRMSQIQAFLGSVPQLTYQLYVSLISAEVPL-GRVVLMVFSLVSVT 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    214 YG----ATLCNMLAIQIKYDDYKIRLGPLEVLCITIWRTLEITSRLLILVLFSATLKLKA 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 VPFLVLNFLILLFE-PWIKFWRSGAQMPNNIEKNFSRVGTLVVLI-----SVTILYAGI 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 NFSCWSALQLRLADRDLVDK------GQNWGHMGLHYSVRLV-ENVIMVLVFKFFGV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            373 KVLLUYCHSLIALQLIIAYLISIDFMLLFFQYLHPLRSLFTHNVVDYLHCVCCHQHPRTR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 4.6%; Score 105.5; DB 2; Length 459; Best Local Similarity 19.0%; Pred. No. 0.4; Matches 82; Conservative 66; Mismatches 146; Indels 137; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 DKPLSLFMHLILLGPVIRCLEAMIKYLTLWKKEEQEEPYVSLTRKKMLIDGEEVLIEWEV 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         392 TIMLT-----GLAMLITALYSL-YMLVTTO-----RGTLTSHII---
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A;Cross-references: GDB:9838088; OMIM:602682
A;Map position: 8q24-8q24
C;Superfamily: thrombospondin type 1 repeat homology
F;408-462/Domain: thrombospondin type 1 repeat homology <THR3>
A;Gene: GDB:BAI1
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	12;		
	Сарв	250	SE 979
1584;	81;	TIWRTLE	VWRYIR
Length	Indels	SPLEVLCIT	SA
DB 2;	98;	YKIRLO	
4.6%; Score 105.5; DB 2; Length 1584; 23.0%; Pred. No. 1.7;	8; Mismatches	ATLCHMLAIQIKYDE	VSSLTLLMLVILY
Query Match Best Local Similarity 23.0%;	Matches 65; Conservative 38; Mismatches 98; Indels 81; Gaps 12;	193 ISAEVPLGRVVLMVFSLVSVTYGATLCNMLAIQIKYDDYKIRLGPLEVLCITIWRTLE 250	935 LSADANMEKATLPSVTLI-VGCGVSSLTLLMLVIIYVSVWRYIRSE 979
Query Match Best Local (Matches	Qy 193	Db 935
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286	1035	337	1087
251ITSRLLILV	980 RSVILINFCLSIISSNALILIGQTQTRNKVMCTLVAAFLHFFFLSSFCWVLTEAWQ 1035	287 KFWRSGAQMPNN-IEKNFSRVGTLVVLISVTILYAGINFSCWSALQLRLADR 337	Db. 1036 SYMAVTGHLRNRLİRKRFLCLGWGLPALVVAİSVGFTKAKGYSTMNY-CWLSL 1087
	980	287	1036
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Search completed: April 1, 2003, 08:49:02 Job time : 52 secs

³³⁸ DLVDKGQNWGHMGLHYSVRLVENVIMVLVPKPFGVK-------VLLNYC--HS 381 g ò

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